

Database version 4.5
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OM protein - protein search, using SW model

Run on: March 14, 2002, 17:06:15 / Search time 10.66 seconds
(without alignments)
24,076 Million cell updates/sec

Filter:
Percent score: 42
Sequence: 1 (DPKOS) 7

Scoring table:
Gapop 10.0, Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 6
Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database: SwissProt_39.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	Prod. No.	Accession
1	39	90.5	200	1	CTN2_RAT
2	36	85.7	198	1	REV_SIVMK
3	35	83.3	161	1	Y255_BUCAI
4	35	83.3	161	1	TRMD_CHUPN
5	25	91.2	200	1	CTN2_HUMAN
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PEP001	7			
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A1	2914742			
12	15-DEC-1998 (rel. 37, created)			
13	15-DEC-1998 (rel. 37, last sequence update)			
14	15-DEC-1998 (rel. 37, last annotation update)			
15	PROSHOLIPASE A2 (35-278) (rel. 34.1.4) (Phosphatidylcholine			
16	2-ACYLHYDROLASE)			
17	Phospholipase transphosphatidyl transferase (human green tree frog (Hyla			
18	ekuragaei), Malawi Chameleon (various Madagascar Malagasy),			
19	Leopardsaur (Squamata: Sceloporus), Serpentes: Colubridae,			
20	Viperidae: Crotalidae, Ifimerosaurus,			
21	2914742b 6702,			
22	(1)			
23	SEQUENCE:			
24	ITSDISE Venn:			
25	MEDLINE 9403047, F. Med 9201034,			
26	Ekuragaei, Hyla, I. Shimodensis Y., Ogawa E., et al. N. Nakamura E.,			
27	Chang C.K., et al. Ohio M.:			
28	"Purification, sequencing and characterization of snake amino acid-			
29	sphingolipid phospholipase A2 isozymes from the green tree frog (Hyla			
30	(green habu snake) venom."			
31	Toxicol. 31:957-967 (1993).			
32	1- FUNCTION: P42 CATALYZES THE CATION DEPENDENT HYDROLYSIS OF THE			
33	2- AYL: 2914742b 6702b 6702b 6702b 6702b 6702b 6702b 6702b 6702b 6702b			
34	1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2O) -> 1-ACYLGLYCERYL-			
35	PHOSPHOCHOLINE + A FATTY ACID AND 1-			
36	1- SMILIARITY: BEL: MGS 1, THE PHOSPHOLIPASE A2 FAMILY.			
37	InterPro: IPRO01211: PLP A2.			
38	pfam: PF00908: phospho_1			
39	PRINTS: PRO0084; PHOLIPASTA2.			
40	ProDom: PD000403; P_P_A2_1.			
41	SMART: SM00085; PA2_1.			
42	PROSITE: PS00198; PA2_HLY_1.			
43	PROSITE: PS00199; PA2_ASP_1.			
44	Hydrolysis: Lipid degradation; Calcium; Multiple; Family; Venom.			
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[illegible]

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 57 1428 POSITION 144
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001 Fokkema et al. (1991). *Accumulation of Saccharomyces* and *Saccharomyces*...

002 NMR (1991) 41(1):1.

003 NMR (1991) 41(1):1.

004 NMR (1991) 41(1):1.

005 NMR (1991) 41(1):1.

006 NMR (1991) 41(1):1.

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